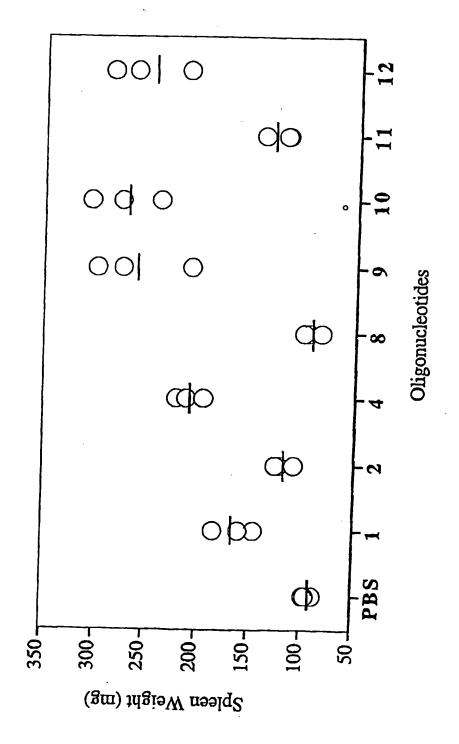
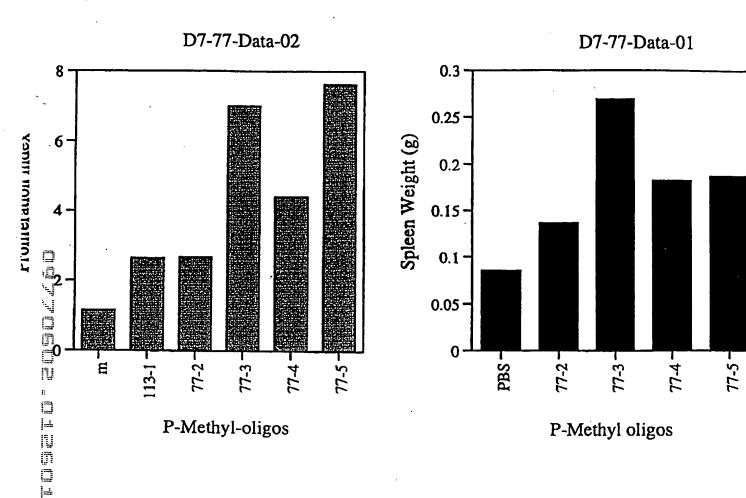


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'IGURE 2

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- 113-1 TCCATGACGTTCCTGATGC
- 77-2 TCCATGACGTTCCTGATGC
- 77-3 TCCATGACGTTCCTGATGC
- 77-4 TCCATGACG TTCCTGATGC
- 77-5 TCCATGACGT TCCTGATGC